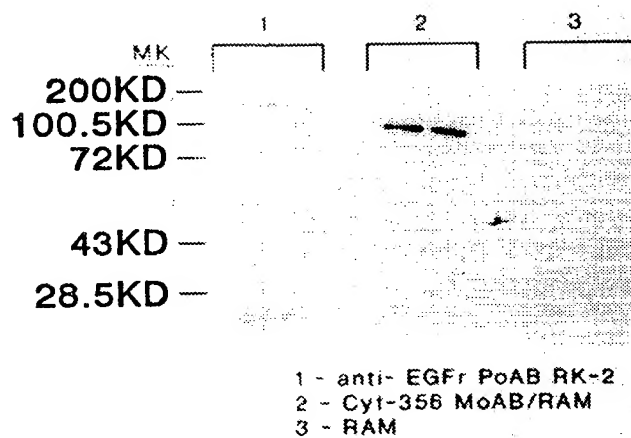


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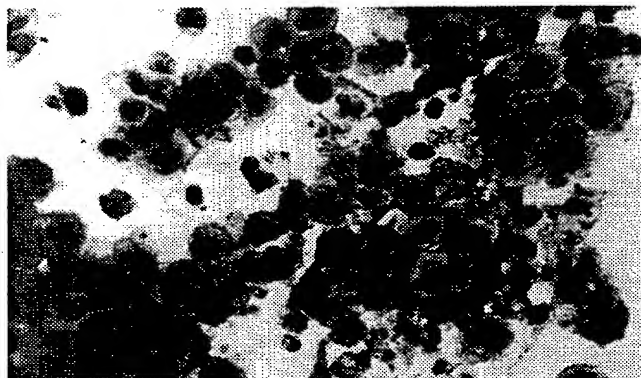
FIGURE 1

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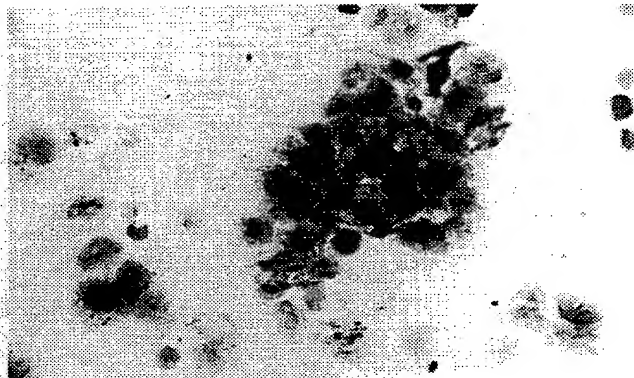
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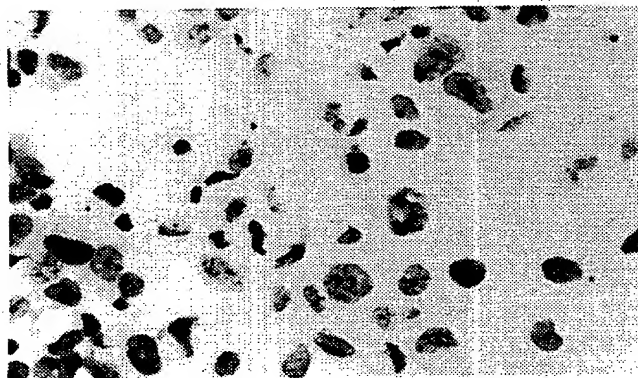
**FIGURE 2A**



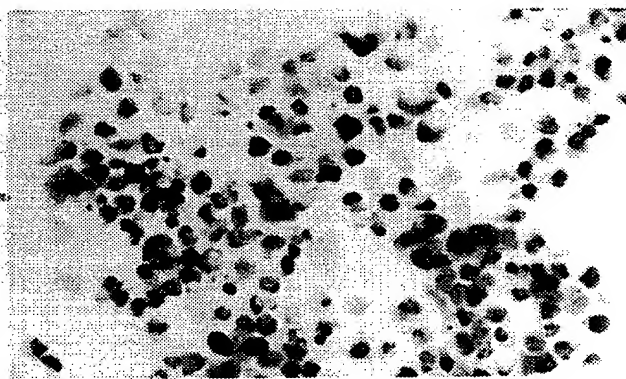
**FIGURE 2B**



**FIGURE 2C**

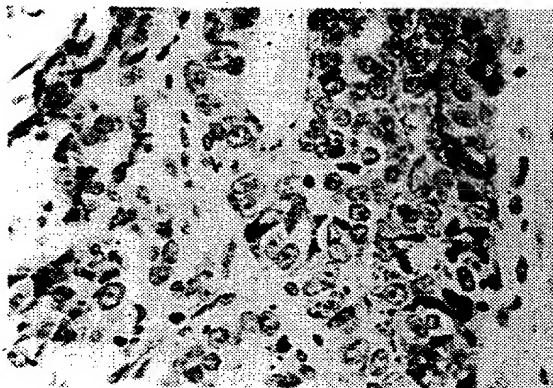


**FIGURE 2D**

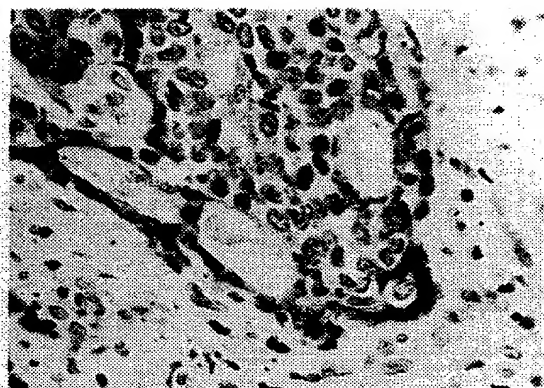


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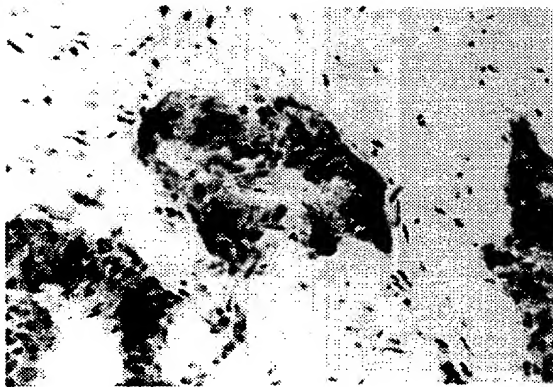
**FIGURE 3A**



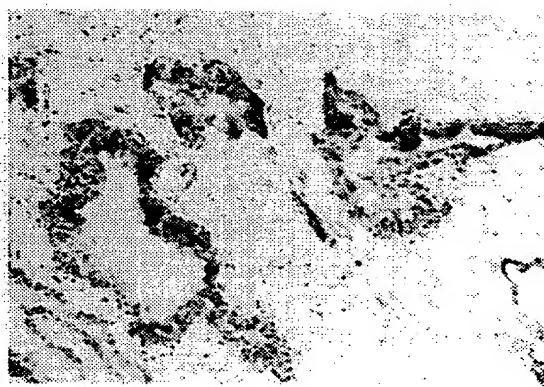
**FIGURE 3B**



**FIGURE 3C**



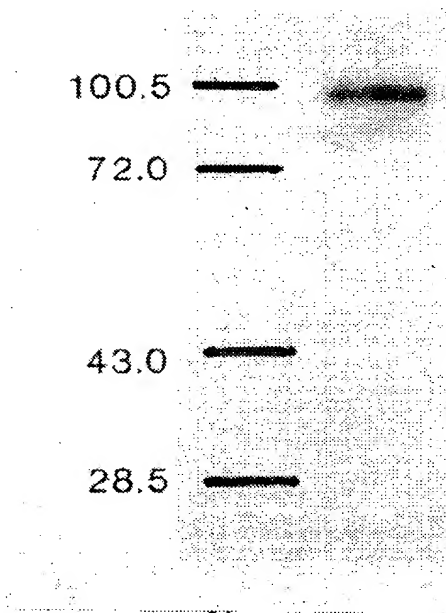
**FIGURE 3D**



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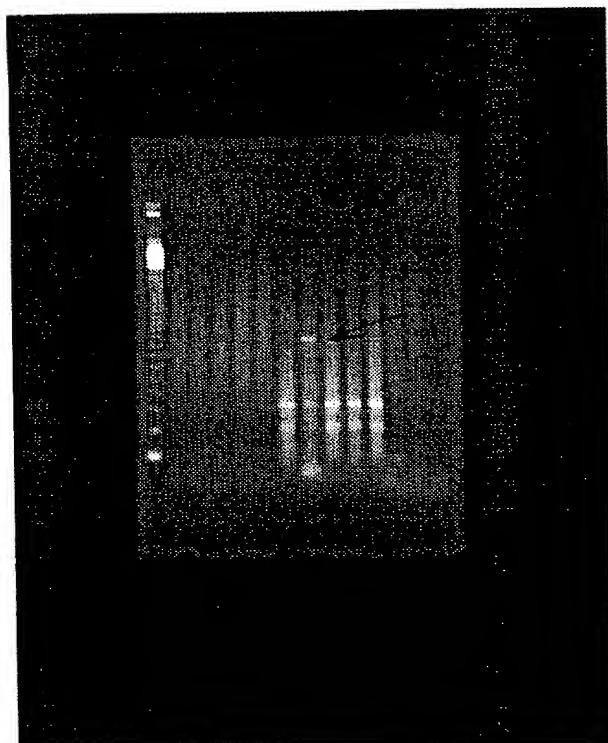
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FIGURE 4



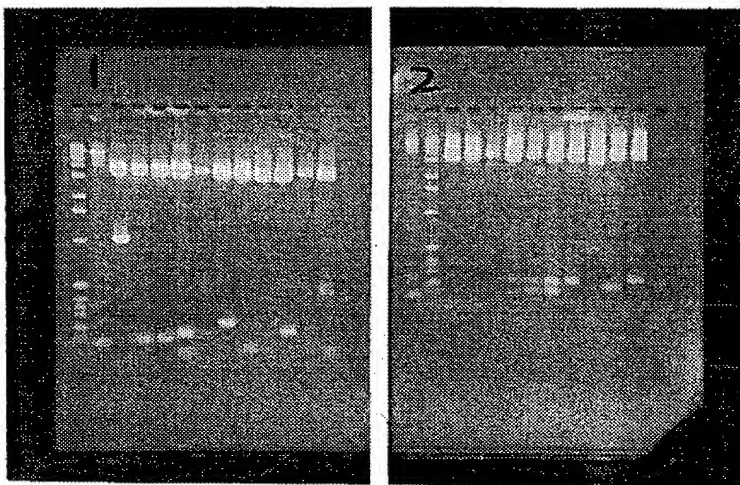
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**FIGURE 5**



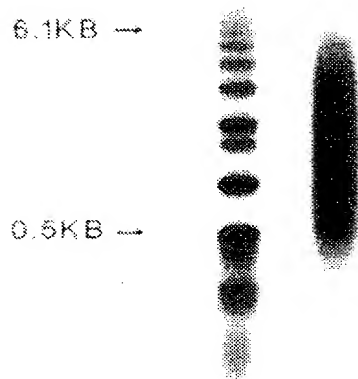
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**FIGURE 6A**    **FIGURE 6B**



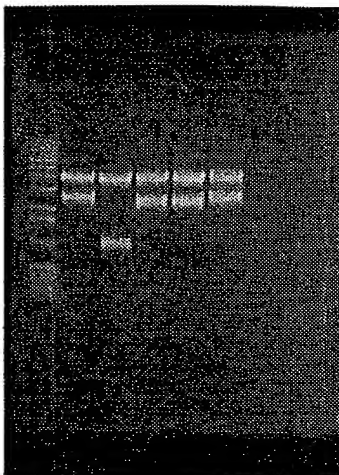
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**FIGURE 7**



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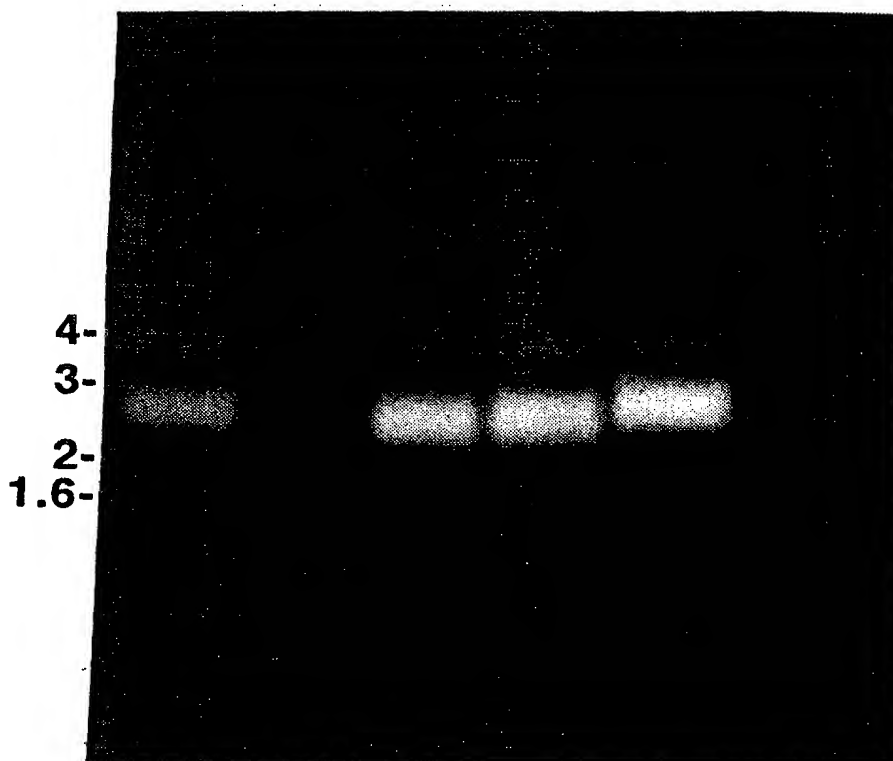
**FIGURE 8**





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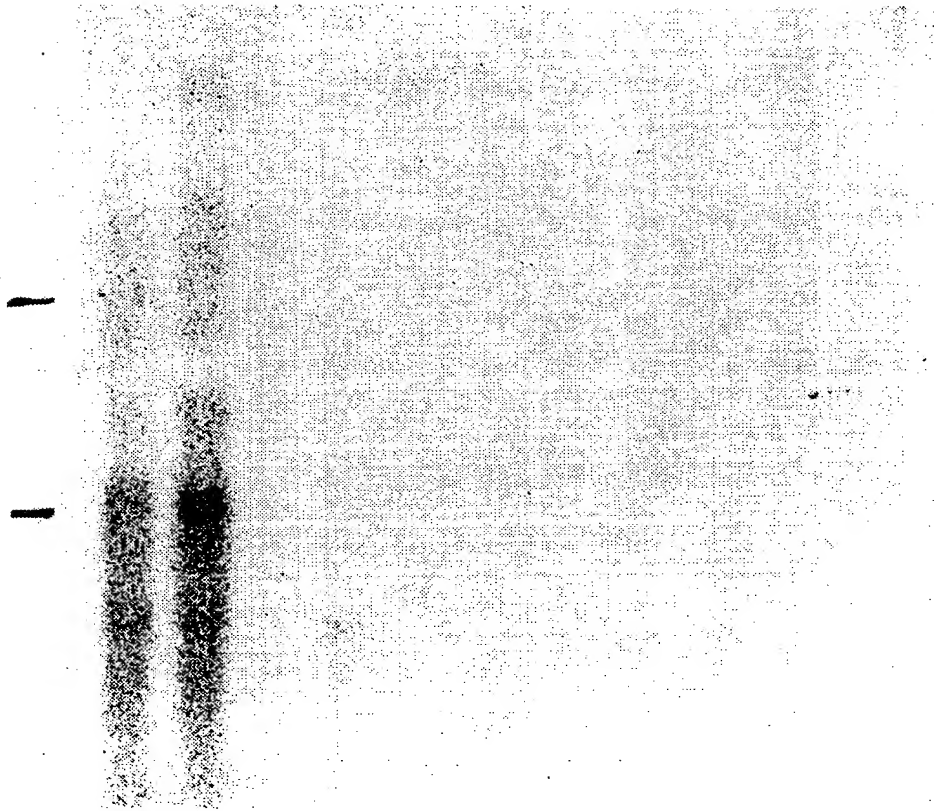
FIGURE 9



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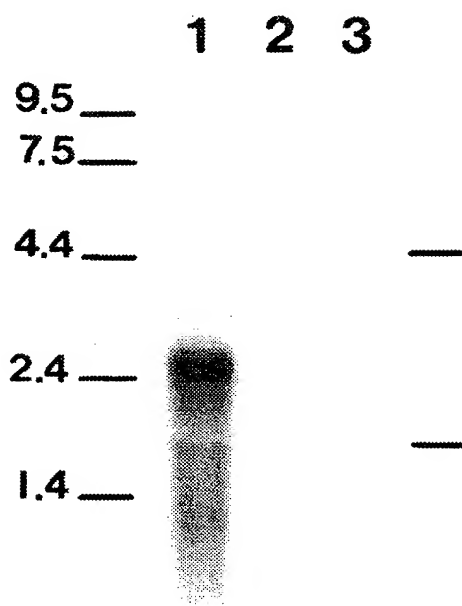
**FIGURE 10**



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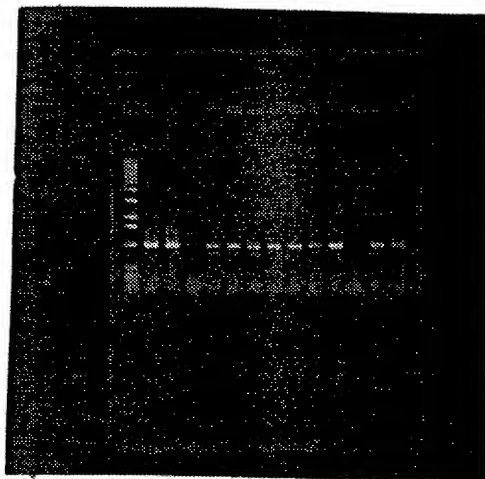
FIGURE 11



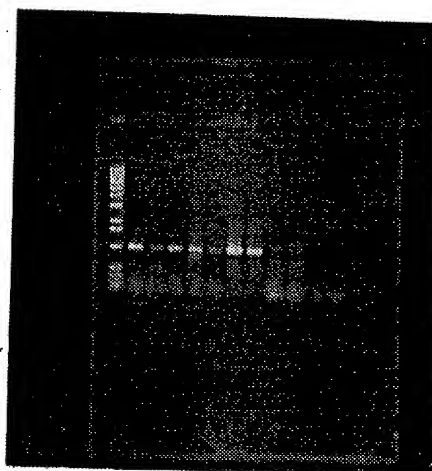
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**FIGURE 12A**

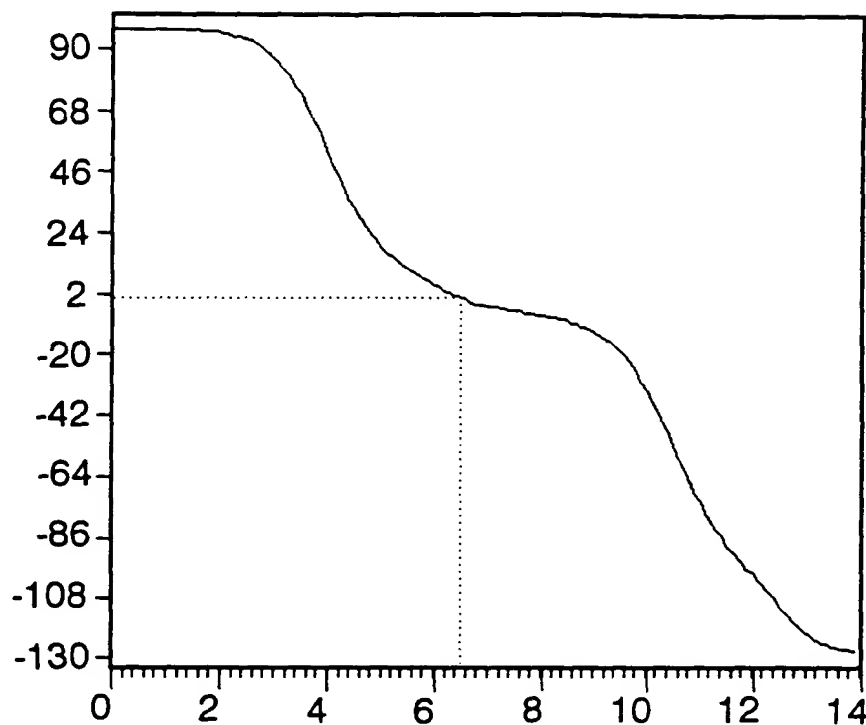


**FIGURE 12B**



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FIGURE 13



**Done on sequence PMSANTIGEN.**

**Total number of residues is: 750.**

**Analysis done on the complete sequence.**

In Helical	(H)	conformation	[DC =	-75	CNAT ] :	264	AA =>	35.2%
In Extended	(E)	conformation	[DC =	-88	CNAT ] :	309	AA =>	41.2%
In Turn	(T)	conformation	[DC =	0	CNAT ] :	76	AA =>	10.1%
In Coil	(C)	conformation	[DC =	0	CNAT ] :	101	AA =>	13.4%

**Sequence shown with conformation codes.**

Consecutive stretch of 5 or more residues in a given conformation are overlined.

[illegible]



### FIGURE 14-3

[illegible]



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FIGURE 14-4

Semi-graphical output.

=====

Symbols used in the semi-graphical representation:

Helical conformation: X      Extended conformation: -  
 Turn conformation: >      Coil conformation: \*

10		20		30		40		50	
MWNLLHETDSAVATARPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEAT									
XXXXXXXXXXXXX-----XXXXXXXXXXXXXXXXXXXXX									
XXXXXXXXXXXXX-----XXXXXXXXXXXXXXXXXXXXX									
60		70		80		90		100	
NITPKHNMKAFDELKAENIKKFLYNFTQIPHLAGTEQNFQIAKQIQSQW									

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FIGURE 14-5

```

XXXXXXXXXXXXXXXXXXXX-->>>-----XXXXXXXXXXXXX-X*--
XXXXXXXXXXXXXXXXXXXX-->>>-----XXXXXXXXXXXXX-X*--

      110      120      130      140      150
      |        |        |        |        |
KEFGLDSVELAHYDVLLSYPNKTHPNYISIIINEDGNEIFNTSLFEPPPG
-->>XXXXXXXXXX-->>>-->>-----*-->>XXXX-->>----->>XXXX>
-->>XXXXXXXXXX-->>>-->>-----*-->>XXXX-->>----->>XXXX>

      160      170      180      190      200
      |        |        |        |        |
YENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKI

```

VIARYGKVFRGNKVNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNLP

[illegible]

GGVQRGNI LNLNGAGDPLTPGYPANEYAYRRGIAEAVGLPSIPVHPIGYY

-----\*-----XX-----\*-----\*-----  
 -----\*-----XX-----\*-----\*-----  
 -----\*-----\*-----\*-----\*-----\*-----  
 -----\*-----\*-----\*-----\*-----\*-----

DAQKLEKMGSA P DSSWRGSLKVPYNVGP GFTGNFSTQKV KMHISTN

```

***-----XXXXXXXXX*-----*----->----->***>-----XXXXXXXXX
***-----XXXXXXXXX*-----*----->----->***>-----XXXXXXXXX
***-----XXXXXXXXX*-----*----->----->***>-----XXXXXXXXX
***-----XXXXXXXXX*-----*----->----->***>-----XXXXXXXXX

```

EVTRIYNVIGTLRGAVEPDRVVI LGGHRDSWVFGIDPQSGAAV VHEIVR



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FIGURE 14-8

LYHSVYETVELVEKFYDPMFKYHLTVAVRGGMVFELANSIVLPFDCRDY

-----XXXXXXXXXXXXXXXXX-X-----XXXXXXXX----->XXX  
 -----XXXXXXXXXXXXXXXXX-X-----XXXXXXXX----->XXX

610            620            630            640            650  
 |            |            |            |            |  
 AVVLRKYADKIYISMKHPQEMKTYSVSFDLSFSAVKNFTEIASKFSERL

XXXXXXXXXX-----X\*XXXXXXXX-----XXXXXXXXXXXXXXXXXXXX  
 XXXXXXXXXXXX-----X\*XXXXXXXX-----XXXXXXXXXXXXXXXXXXXX

660            670            680            690            700  
 |            |            |            |            |  
 QDFDKSNPIVLRMMNDQLMCLERAFIDPLGLPDRPFYRHHVIYAPSSHNY

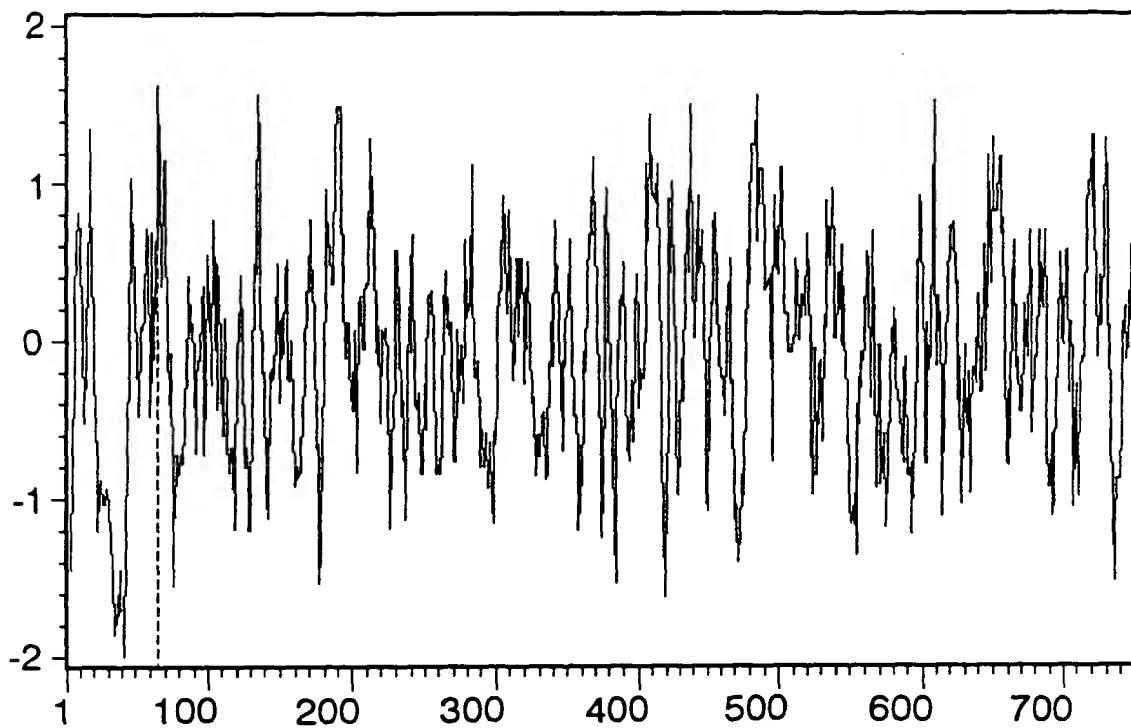
XX>>>\*-----XXXXXXXXXX-->>\*\*\*>----->\*\*\*>  
 XX>>>\*-----XXXXXXXXXX-->>\*\*\*>----->\*\*\*>

710            720            730            740            750  
 |            |            |            |            |  
 AGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAFTVQAAETLSEVA

----->-----XXXXXXXX\*\*XXXXXXXXX-----XXXXXXXXXXXXXXXX  
 ----->-----XXXXXXXX\*\*XXXXXXXXX-----XXXXXXXXXXXXXXXX

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FIGURE 15A



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## FIGURE 15B

\*\*\*\*\*  
 \* PREDICTION OF ANTIGENIC DETERMINANTS \*  
 \*\*\*\*\*

Done on sequence PMSANTIGEN.

Total number of residues is: 750.

Analysis done on the complete sequence.

The method used is that of Hopp and Woods.

The averaging group length is: 6 amino acids.

-> This is the value recommended by the authors <-

-----

The three highest points of hydrophilicity are:

( 1 )	Ah= 1.62	: From	63 to	68	: Asp-Glu-Leu-Lys-Ala-Glu
( 2 )	Ah= 1.57	: From	132 to	137	: Asn-Glu-Asp-Gly-Asn-Glu
( 3 )	Ah= 1.55	: From	482 to	487	: Lys-Ser-Pro-Asp-Glu-Gly

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 100% of the cases assigned to a known antigenic group. The second and third point: gave a proportion of 33% of incorrect predictions.

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FIGURE 16-1

The best scores are:

	G.gallus mRNA for transferrin receptor	initn	init1	opt
CHKTFER		203	120	321
RATTRFR	Rat transferrin receptor mRNA, 3' end.	164	164	311
HUMTFRR	Human transferrin receptor mRNA, complete cd	145	145	266

CHKTFER G.gallus mRNA for transferrin receptor 203 120 321  
51.9% identity in 717 nt overlap

1020	1030	1040	1050	1060	1070
pmsgen	TGTCACGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCCTCTCACACCAGGTTA				

CHKTFE	TACACTTATCCCATTCGGACATGCCACCTTGGAACTGGAGACCCCTTACACCCAGGCTT				
990	1000	1010	1020	1030	1040

1080	1090	1100	1110	1120	1130
pmsgen	CCCAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAAGTAT				

CHKTFE	CCCTTCGTTCAACCCACACCCA---GTTCCACCAAGTTGAATCTTCAGGACTACCCACAT				
1050	1060	1070	1080	1090	1100

1140	1150	1160	1170	1180	1190
pmsgen	TCCTGTTCAATCCAAATGGATACATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTC				

CHKTFE	TGCTGTTCAGACCATCTCTAGCAGTGCAGCAGCCAGGCTGTTTCAGCAAAATGGATGGAGA				
1110	1120	1130	1140	1150	1160





### FIGURE 16-3

[illegible]

```

1500      1510      1520      1530      1540      1550
pmsgen  ACCTAGAAGAACAAATTTTGTTCAGAGCTGGGATGCAGAGAAATTGGTCTTCTTGCTTC
        ::: :: ::: : X:::: ::::: ::::: ::::: ::::: ::::: :::::
CHKTFE  ACCGAGGCGAAGCATCATCTTTGCTAGCTGGAGTGCAGGAGACTACGGAGCTGTGGGTGC
1450      1460      1470      1480      1490      1500

```

	1560	1570	1580	1590	1600	1610
pmngen	TACTGAGTGGCAGAGGAGAA	TTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTA				
	::::: ::	::::: ::	: ::	: ::	: ::	: ::
CHKTFE	TACTGAATGGCTGGAGGGGTACTCTGCCATGCTGCATGCCAAAGCTTTCACCTTACATCA					
	1510	1520	1530	1540	1550	1560

```

1620      1630      1640      1650      1660      1670
pmsgen  TGC-TGACTCATCTATAGAAAGGAACTA-CACTCTGAGAGTTGATTGTACACCGCTGATG
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
CHKTFE  -GCTTGGATGCTCCAGTCCCTGGGAGCAAGCCATGTCAAGATTCTGCCAGCCCCCTTGCTG
1570      1580      1590      1600      1610      1620

```







FIGURE 16-7

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1550	1560	1570	1580	1590	1600
pmsgen	CTTGGTTCTACTGAGTGGGCAGAGGAGAA---	TTCAAGACTCCTTCAAGAGCGTGGCGTG			
	::::: : ::::::::::: ::::: : X ::::: : ::::: : ::::: : ::::: :				
RATTRF	GTTGGTCCGACTGAGTGGCTGGAGGGGTACCTTTTCATCTTTGCATCTAAAG---	GCATTTC			
970	980	990	1000	1010	1020
1610	1620	1630	1640	1650	1660
pmsgen	GCTTATATTAATGCTGACTCATCTATAGAAAGAACTA-C	ACTCTGAGAGTTGATGTAC			
	::::: : ::::::::::: ::::: : : ::::: : ::::: : ::::: : ::::: :				
RATTRF	ACTTACATTAAT-CTGGATAAAGTCGTCCTGGGTACTAGCAACTTCAAGGTTTCTGCCAG				
1030	1040	1050	1060	1070	1080
1670	1680	1690	1700	1710	1720
pmsgen	ACCGCTGATGTACAGCTTGGTACACAACTTAACAAAGAGCTGAAAGC-CCTGATGAAG				
	::: : : ::::: : : ::::: : ::::: : ::::: : ::::: : ::::: :				
RATTRF	CCCCCTATTATATACACTTATGGGGAAGATAATGCAGGA--CGTAAAGCATCCGA-----				
1090	1100	1110	1120	1130	

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FIGURE 16-8

```

1730      1740      1750      1760      1770
pmsgen  GCTTTGAAGGCAAAATCTCTTTAT-GAA-----AGTTGGACTAAATAAGTCCCTTCCCCCAG
          :::: :: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RATTRF  ---TTGATGGAAATATCTATATCGAAACAGTAATTGGATTAGCAAAATTGAGGAACTTT
1140      1150      1160      1170      1180      1190

1780      1790      1800      1810      1820      1830
pmsgen  AGTTCAGTGGCATGCCAGGATAAGCAAATTGGGATCTGGAAATGATTTTGAGGTGTCTCT
          CCTTGGACAAATGCTGCATTCCCTTTTCTTGCCATATTCAGGAATCCCAGCAGTTTCTTTCT
1200      1210      1220      1230      1240      1250

```

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```

1400      1410      1420      1430      1440      1450
pmsgen CCGGACTCATGGGTGTTGGTGGTATTGACCCCTCAGAGT-GGAGCAGCTGTTGTTTCATG
      : : : : : : : : : : : : : : : : : :
HUMTFR GAGAGATGCATGGGGCCCTGGAGCTGCAAATC-CGGTGTAGGCACAGCTCTCCTATTGA
1320      1330      1340      1350      1360      1370

```



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FIGURE 16-10

```
1460      1470      1480      1490      1500
pmsgen AAATTG---TGAGGAGCTTTGGAACACTGAAAGGAAGGTGGAGACCTAGAAGACAA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
HUMTFR AACTTGCCAGATGTTCTCAGATATGGTCTTAAAGATGGGTTTCAGCCCGCAGCAAGCA
1380      1390      1400      1410      1420      1430

1510      1520      1530      1540      1550      1560
pmsgen TTTGTGTTGCAAGCTGGGATGCAGAAGAAATTGGTCTTCTTGGTCTACTGAGTGGGCAG
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
HUMTFR TTATCTTTGCCAGTTGGAGTGCTGGAGACTTTGGATCGGTGGTGCCACTGAATGGCTAG
1440      1450      1460      1470      1480      1490

1570      1580      1590      1600      1610      1620
pmsgen A-GGAGAAATTCAGACTCCTTCAAGAGCGTGGCGTTGCTTATATTAATGCTGACTCATCT
      : :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HUMTFR AGGATACCTTTCGTC-CCTGCATTAAAGGCTTTCACCTTATATTAATCTGGATAAAGCG
1500      1510      1520      1530      1540      1550

1630      1640      1650      1660      1670      1680
pmsgen ATAGAAGAAACTACACTCTGAGAGTTGATGTACACCGCTGATGTACA-GCTTGGT-AC
      : :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HUMTFR GTTCTTGGTACCAGCAACTTCAAGGTTTCTGCCAGCCCACTGTTGTATACGCTTATTGAG
1560      1570      1580      1590      1600      1610
```

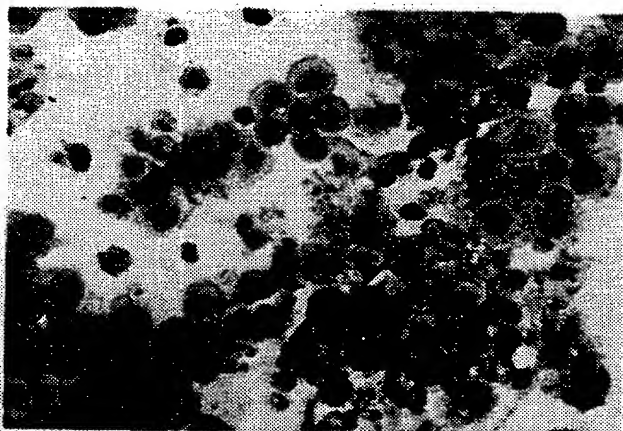
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**FIGURE 16-11**

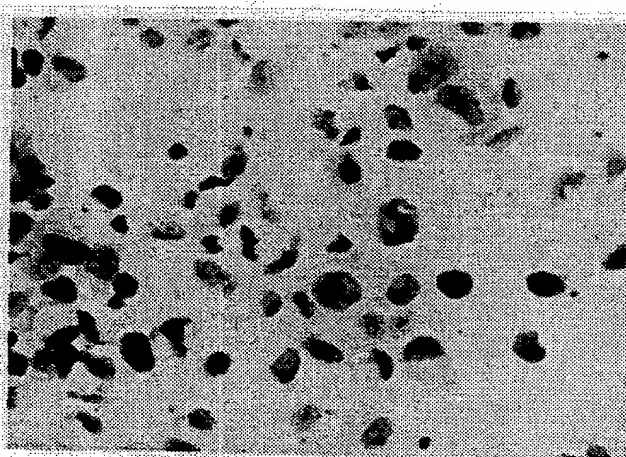
	1690	1700	1710	1720	1730	1740
pmsgen	ACAACCTAACAAAGAGCTGAAAGCCCTGATGAAGGCTTTGAAGGCAAACTCTTTATG					
	:	:	:	:	:	:
HUMTER	AAAACAATGCCAAATGTGAAGCATCCGGTTACTGGGCAATTTCTATATCAGGACAGCAAC					
	1620	1630	1640	1650	1660	1670

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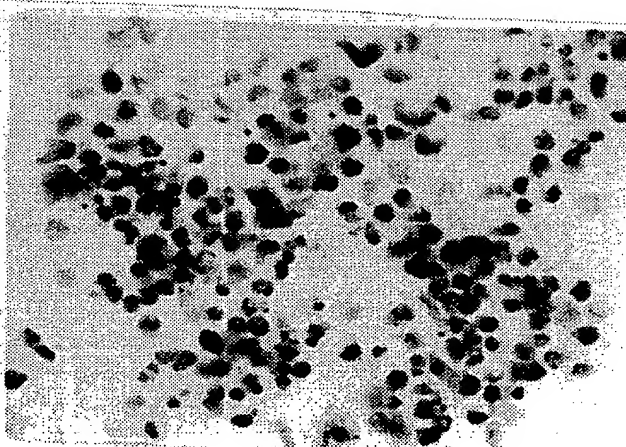
**FIGURE 17A**



**FIGURE 17B**

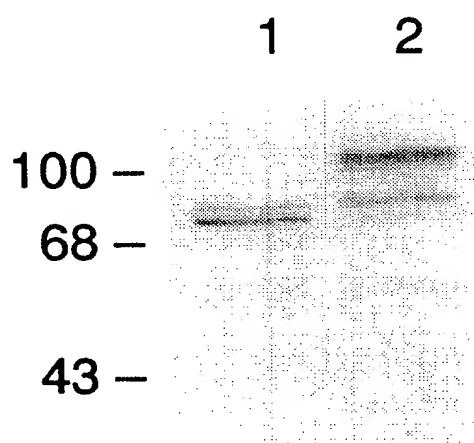


**FIGURE 17C**



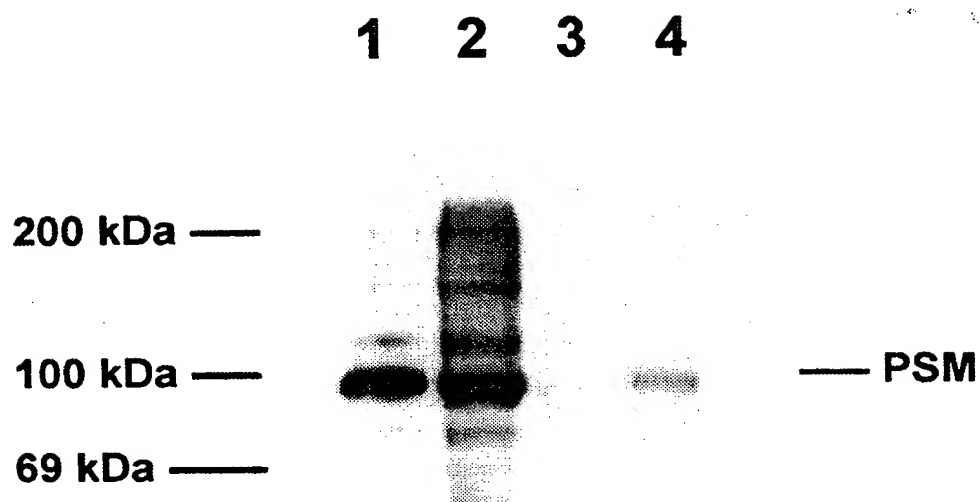
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FIGURE 18



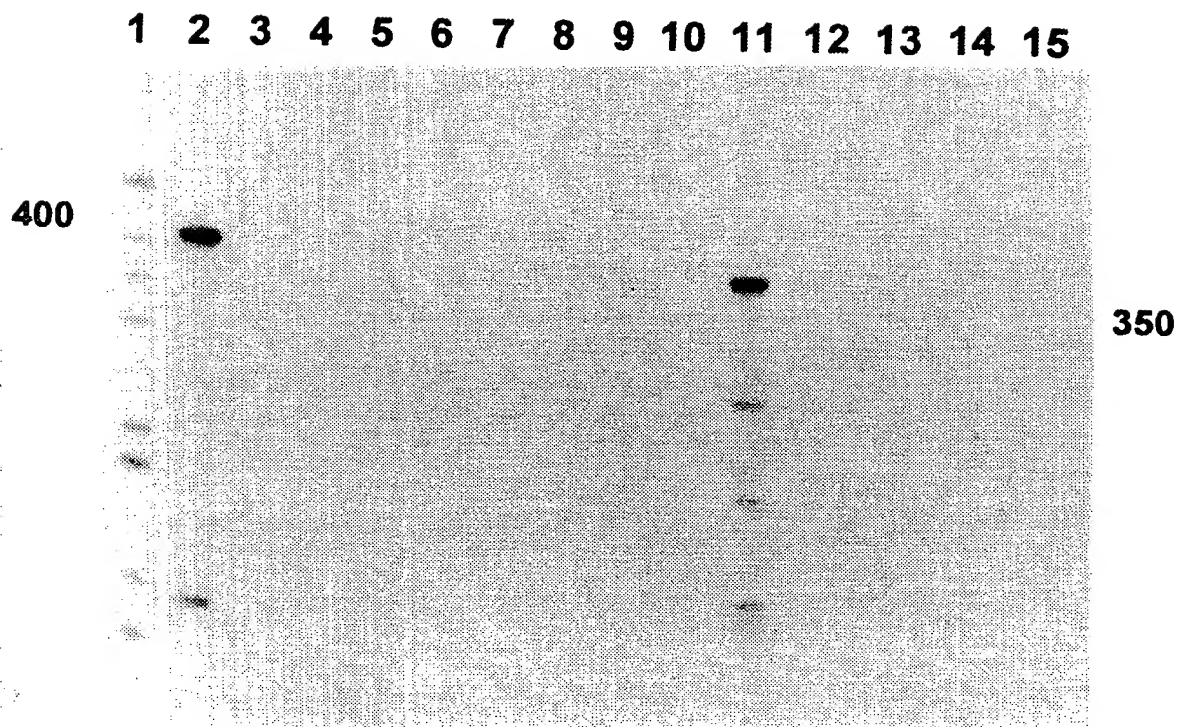
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FIGURE 19



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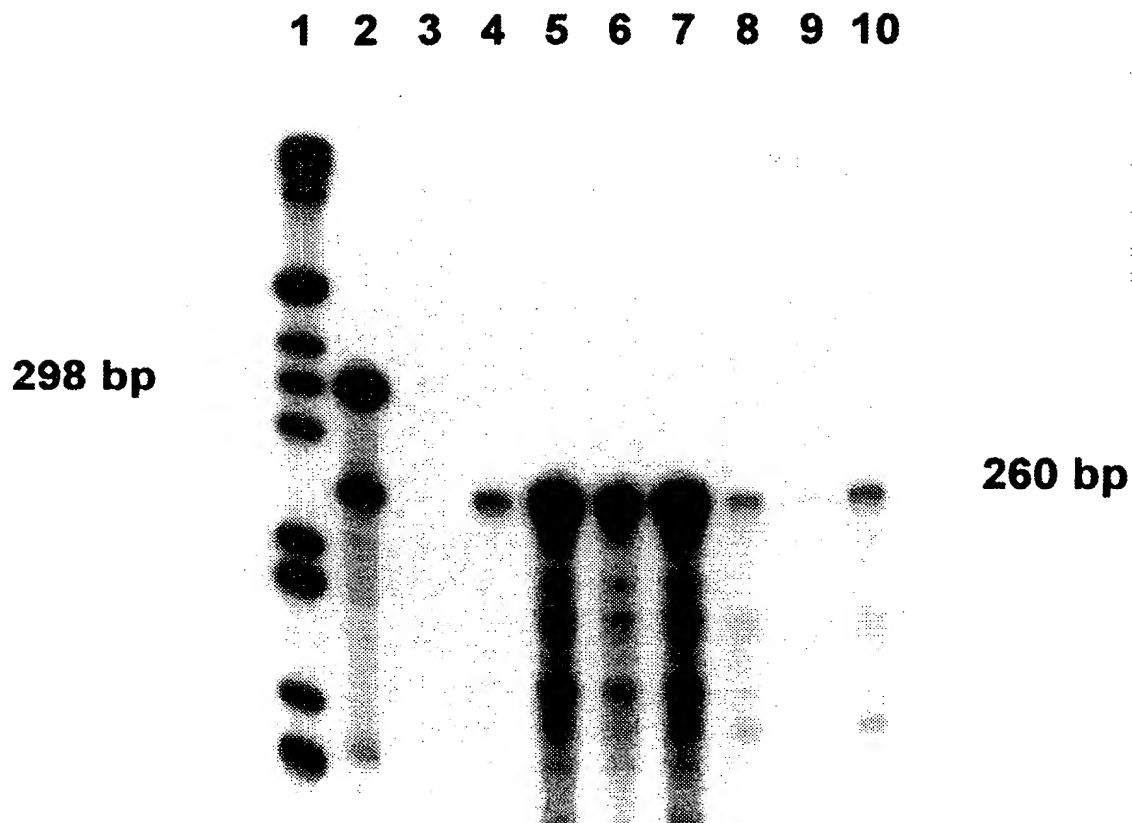
FIGURE 20





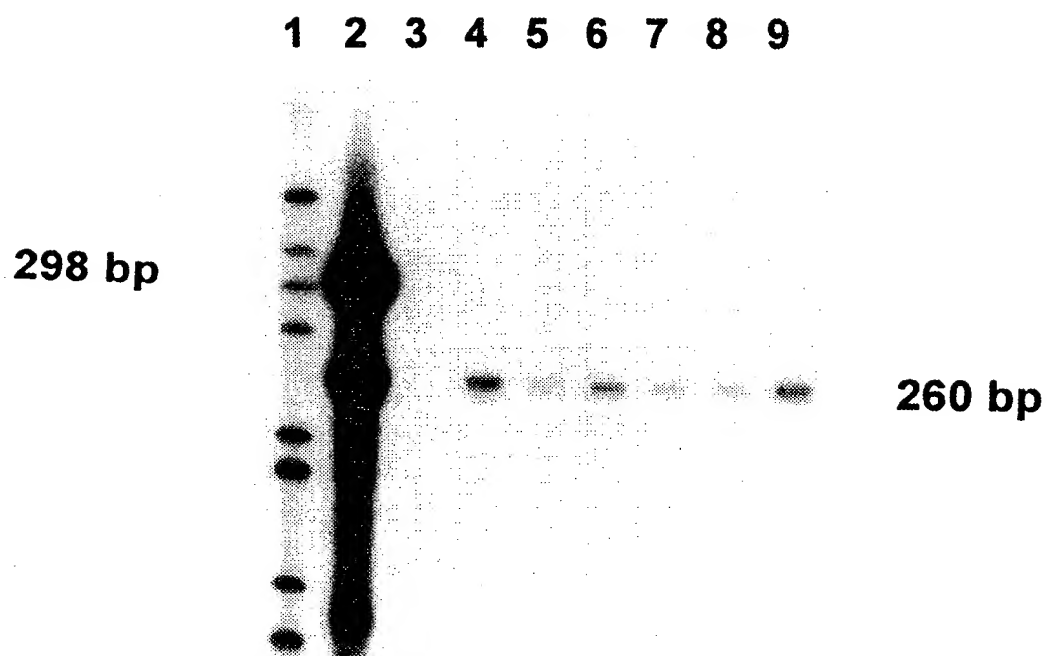
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FIGURE 21



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FIGURE 22





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**FIGURE 23**

CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	-	-
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	-	-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	-	-
R1564 (RAT MAMMARY)	NO	YES	-	-
R1564-11-c14	YES	YES	-	+
R1564-11-c15	YES	YES	-	REPEAT
R1564-11-c16	YES	YES	-	ND
R1564-11-c12	YES	YES	ND	+

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FIGURE 24A

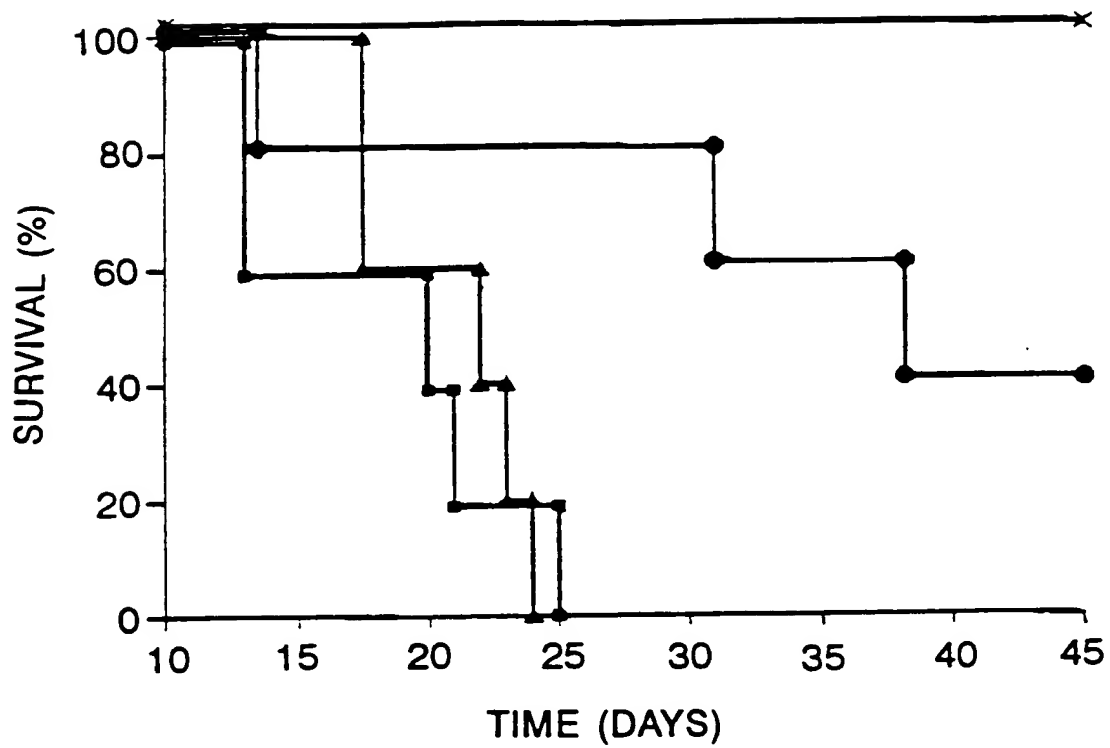
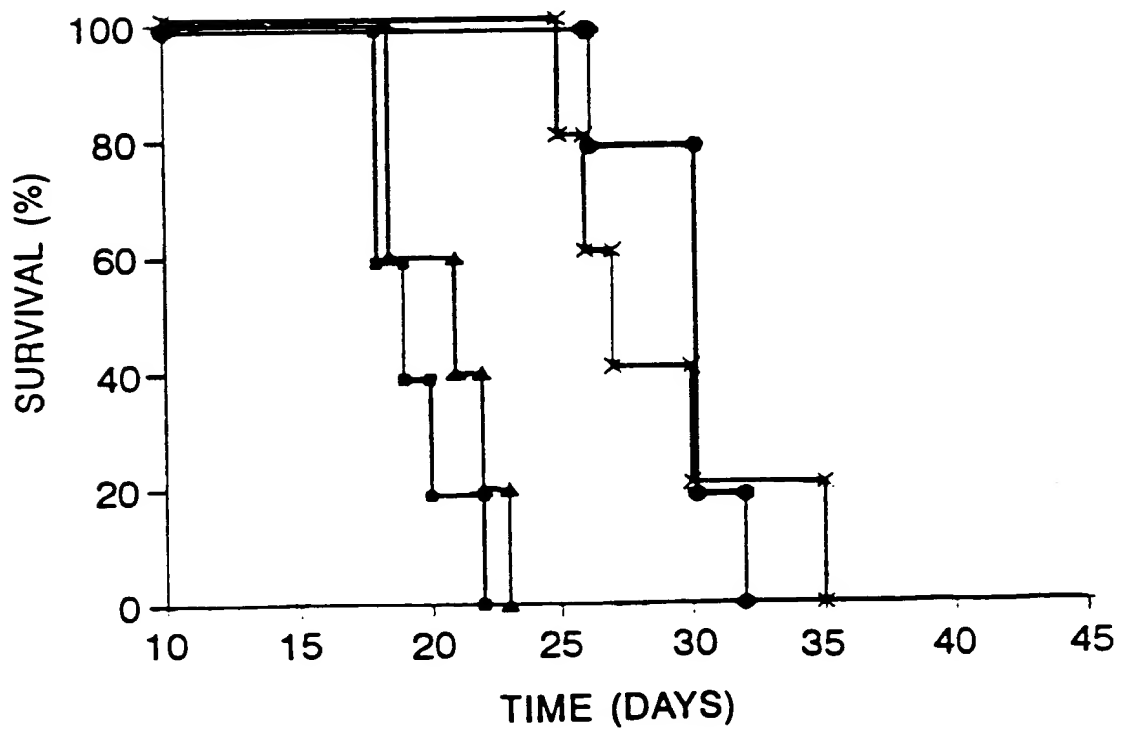


FIGURE 24B



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FIGURE 25A

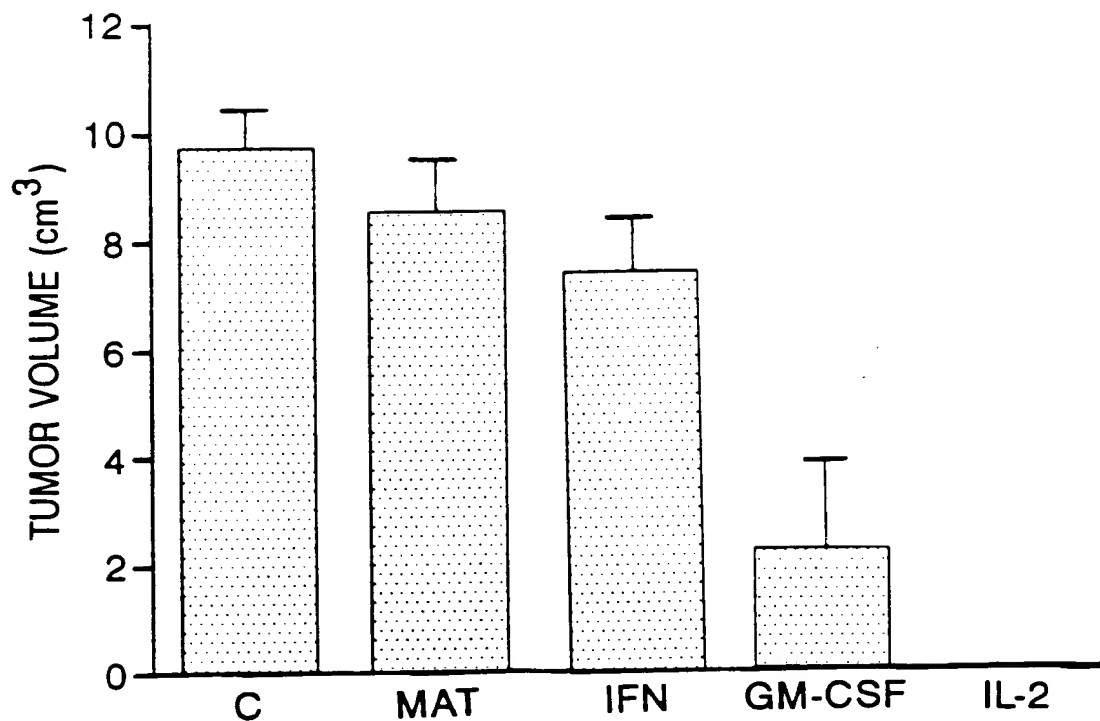
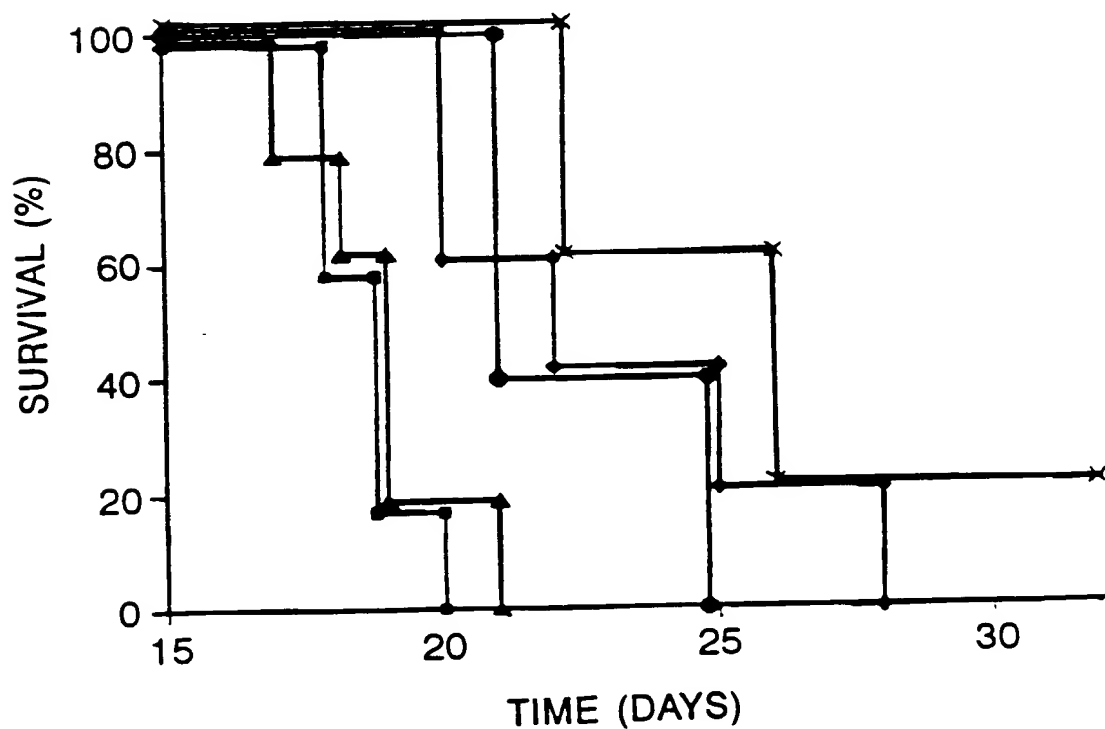
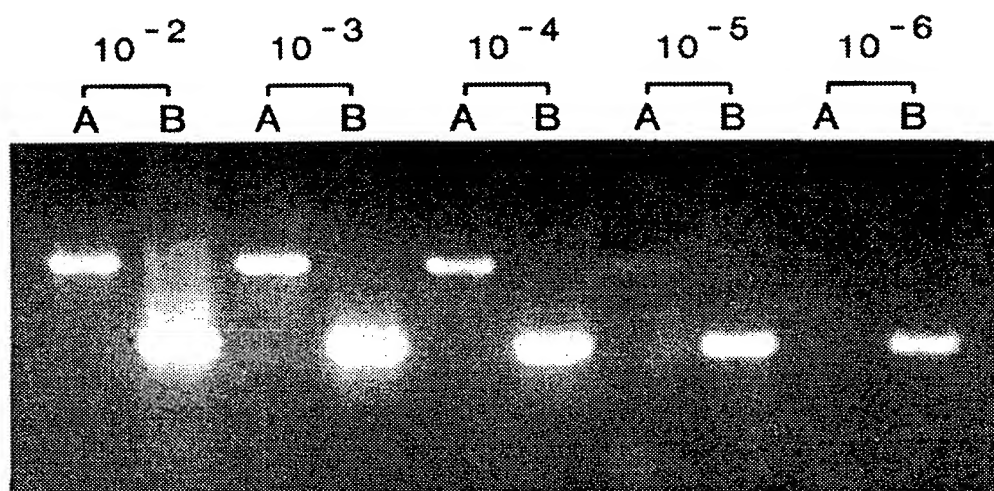


FIGURE 25B



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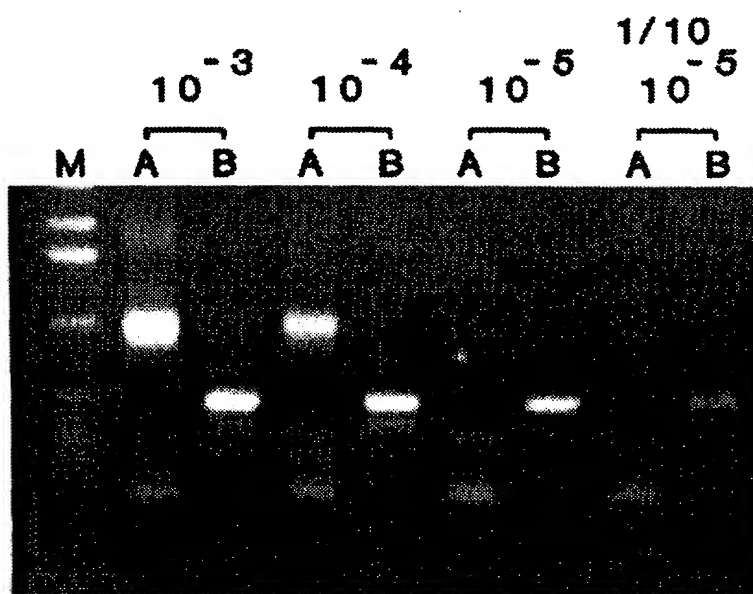
FIGURE 26



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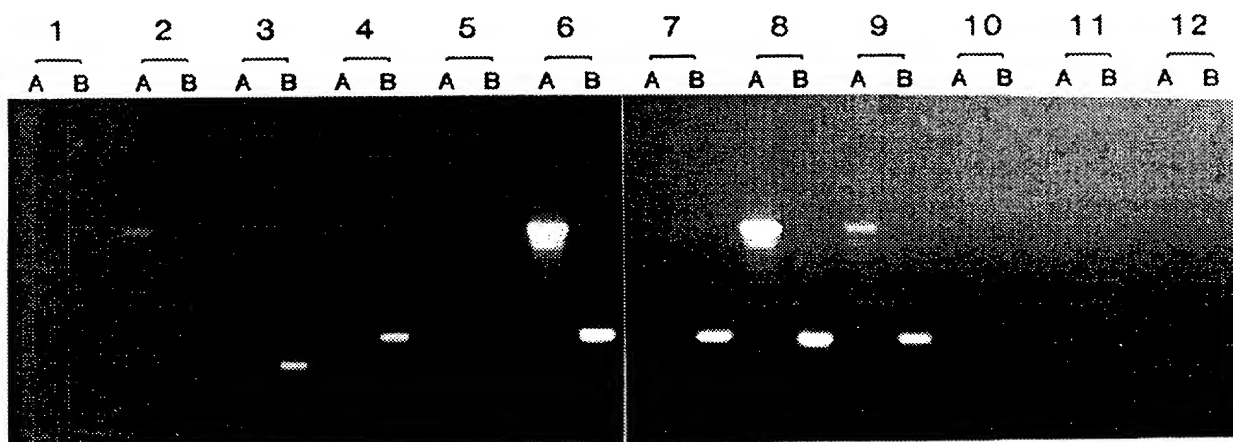
FIGURE 27



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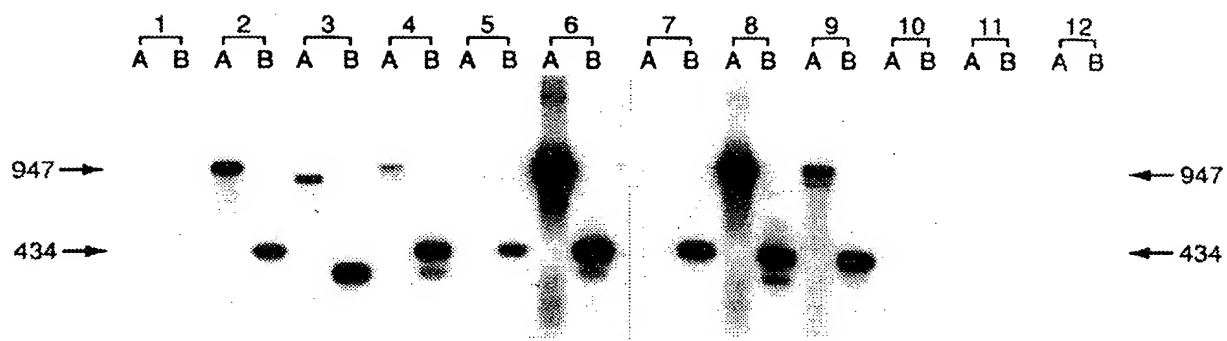
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FIGURE 28



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FIGURE 29



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FIGURE 30

Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	-	+
2	T2NoMo	RRP 7/93	6.1	-	-	+
3	T2CNoMo	PLND 5/93	4.5	0.1	-	+
4	T2BNoMo	RRP 3/92	NMA	0.4	-	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	-	+
6	Recur T3	I-125 1986	54.7	1.4	-	+
7	T3ANoMo	RRP 10/92	NMA	0.3	-	+
8	T3NxMo	XRT 1987	7.5	0.1	-	-
9	T3NxMo	Proscar + Flutamide	35.4	0.7	-	-
10	D2	S/P XRT Flutamide + Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5	-	+
13	T3NoMo	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	-	-
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	-
15	D1	Proscar + Flutamide	20.8	0.5	-	-
16	T2CNoMo	RRP 4/92	0.1	0.3	-	-